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30. The method of Claim 29, wherein the first cistron encodes CREB variant Y134F.

31. The method of Claim 22, wherein the first cistron encodes a CREB protein or a variant thereof, and the second cistron encodes a Bcl-2 protein or a Bcl-2 protein having a deletion in the regulatory loop domain.

32. The method of Claim 22, wherein the first cistron encodes a variant El a protein with a mutation in CR1, and the second cistron encodes an Elb-19K protein, a Bcl-2 protein, or a Bcl-2 protein having a deletion in the regulatory loop domain.

33. The method of Claim 22, wherein the second cistron encodes an apoptosis-protective protein selected from the group consisting of a dominant negative mutant of p53, a protein that interacts with BAX, a protein that interacts with BAK, an inhibitor of apoptosome formation, and a downstream apoptosis inhibitor.

34. The method of Claim 22, wherein the second cistron encodes an adenovirus Elb-19K protein, a Bcl-2 protein, or a Bcl-2 protein having a deletion in the regulatory loop domain.

35. The method of Claim 22, wherein said polypeptide is a single-chain antibody or a heavy or light chain of an antibody or antibody fragment.

36. The method of Claim 22, wherein said polypeptide is a part of a library of polypeptides.

37. A mammalian host cell for recombinant polypeptide expression comprising a first cistron encoding a transactivator protein and a second cistron encoding an apoptosis-protective protein that prevents cell-killing due to expression of the transactivator protein.

38. The host cell of Claim 37, further comprising a third cistron encoding one or more desired polypeptide under the control of a promoter responsive to the transactivator protein.

39. The host cell of Claim 37, wherein the third cistron is associated with a ubiquitous chromatin opening element, an insulator, or a barrier element.

40. The host cell of Claim 37, wherein the transactivator protein is expressed from an efficient heterologous promoter.

MAQAGRTGYDNREIVMKYIHYKLSQRGYEWVDVGDVDAAPLG  
AAPTPGIFSFPESNPTPAVHRDMAARTSPLRPIVATTGPT  
LSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTA  
RGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS  
PLVDNIALWMTEYLNRLHTWIQDNGGWDAFVELYGPSVRP  
LFDFSWLSLKTLLSLALVGACITLGTYLGHK (SEQ  
ID NO: 1)

**FIG. 1**

MAQAGRTGYDNREIVMKYIHYKLSQRGYEWVDVGDVDA**AAA**  
**ASP**VPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTA  
RGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS  
PLVDNIALWMTEYLNRLHTWIQDNGGWDAFVELYGPSVRP  
LFDFSWLSLKTLLSLALVGACITLGTYLGHK (SEQ  
ID NO: 2)

**FIG. 2**

1 ATGGCTCAAG CTGGGAGAAC AGGGTATGAT AACCGAGAGA TCGTGATGAA  
51 GTACATCCAT TATAAGCTGT CACAGAGGGG CTACGAGTGG GATGTGGGAG  
101 ATGTGGACGC CGCGGCCGCG GCCGCGAGCC CCGTGCCACC TGTGGTCCAC  
151 CTGACCCTCC GCCGGGCTGG GGATGACTTC TCCCGTCGCT ACCGTCGCGA  
201 CTTCGCGGAG ATGTCCAGTC AGCTGCACCT GACGCCCTTC ACCGCGAGGG  
251 GACGCTTTGC TACGGTGGTG GAGGAACTCT TCAGGGATGG GGTGAACTGG  
301 GGGAGGATTG TGGCCTTCTT TGAGTTCGGT GGGGTCATGT GTGTGGAGAG  
351 CGTCAACAGG GAGATGTCAC CCCTGGTGGA CAACATCGCC CTGTGGATGA  
401 CCGAGTACCT GAACCGGCAT CTGCACACCT GGATCCAGGA TAACGGAGGC  
451 TGGGACGCAT TTGTGGA ACT GTACGGCCCC AGTGTGAGGC CTCTGTTTGA  
501 TTTCTCTTGG CTGTCTCTGA AGACCCTGCT CAGCCTGGCC CTGGTCGGGG  
551 CCTGCATCAC TCTGGGTACC TACCTGGGCC ACAAGTGA (SEQ ID NO: 3)

**FIG. 3**

MRHIICHGGVITEEMAASLLDQLIEEVVLADNLPPPSHFE  
PPTLHELHDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGI  
DLLTFPPAPGSPEPPHLSRQPEQPEQRALGPVSMPNLVP  
EVIDLTGHEAGFPPSDDDEDEEGEEFVLDYVEHPGHGCR  
SCHYHRRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPE  
PEPEPEPARPTRRPKMAPAILRRPTSPVSRECNSSTDSCD  
SGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDL  
LNEPGQPLDLCKRPRP (SEQ ID NO: 4)

FIG. 4

1 ATGAGACATA TTATCTGCCA CGGAGGTGTT ATTACCGAAG AAATGGCCGC  
 51 CAGTCTTTTG GACCAGCTGA TCGAAGAGGT ACTGGCTGAT AATCTTCCAC  
 101 CTCCTAGCCA TTTTGAACCA CCTACCCTTC ACGAACTGCA TGATTTAGAC  
 151 GTGACGGCCC CCGAAGATCC CAACGAGGAG GCGGTTTCGC AGATTTTTCC  
 201 CGACTCTGTA ATGTTGGCGG TGCAGGAAGG GATTGACTTA CTCACTTTTC  
 251 CGCCGGCGCC CGGTTCTCCG GAGCCGCCTC ACCTTTCCCG GCAGCCCGAG  
 301 CAGCCGGAGC AGAGAGCCTT GGGTCCGGTT TCTATGCCAA ACCTTGTACC  
 351 GGAGGTGATC GATCTTACCG GCCACGAGGC TGGCTTTCCA CCCAGTGACG  
 401 ACGAGGATGA AGAGGGTGAG GAGTTTGTGT TAGATTATGT GGAGCACCCC  
 451 GGGCACGGTT GCAGGTCTTG TCATTATCAC CGGAGGAATA CGGGGGACCC  
 501 AGATATTATG TGTTGCTTTT GCTATATGAG GACCTGTGGC ATGTTTGTCT  
 551 ACAGTAAGTG AAAATTATGG GCAGTGGGTG ATAGAGTGGT GGGTTTGGTG  
 601 TGGTAATTTT TTTTAAATT TTTACAGTTT TGTGGTTTAA AGAATTTTGT  
 651 ATTGTGATTT TTTTAAAAGG TCCTGTGTCT GAACCTGAGC CTGAGCCCGA  
 701 GCCAGAACCG GAGCCTGCAA GACCTACCCG CCGTCCTAAA ATGGCGCCTG  
 751 CTATCCTGAG ACGCCCGACA TCACCTGTGT CTAGAGAATG CAATAGTAGT  
 801 ACGGATAGCT GTGACTCCGG TCCTTCTAAC ACACCTCCTG AGATACACCC  
 851 GGTGGTCCCG CTGTGCCCCA TTAAACCAGT TGCCGTGAGA GTTGGTGGGC  
 901 GTCGCCAGGC TGTGGAATGT ATCGAGGACT TGCTTAACGA GCCTGGGCAA  
 951 CCTTTGGACT TGAGCTGTAA ACGCCCCAGG CCATAA (SEQ ID NO: 5)

**FIG. 5**

1 GAATTCGCCG CCACCATGGA GGCTTGGGAG TGTTTGGAAG ATTTTCTGC  
51 TGTGCGTAAC TTGCTGGAAC AGAGCTCTAA CAGTACCTCT TGGTTTTGGA  
101 GGTTCCTGTG GGGCTCATCC CAGGCAAAGT TAGTCTGCAG AATTAAGGAG  
151 GATTACAAGT GGGAATTTGA AGAGCTTTTG AAATCCTGTG GTGAGCTGTT  
201 TGATTCTTTG AATCTGGGTC ACCAGGCGCT TTTCCAAGAG AAGGTCATCA  
251 AGACTTTGGA TTTTCCACA CCGGGGCGCG CTGCGGCTGC TGTGCTTTT  
301 TTGAGTTTTA TAAAGGATAA ATGGAGCGAA GAAACCCATC TGAGCGGGGG  
351 GTACCTGCTG GATTTTCTGG CCATGCATCT GTGGAGAGCG GTTGTGAGAC  
401 ACAAGAATCG CCTGCTACTG TTGTCTTCCG TCCGCCCCGC GATAATACCG  
451 ACGGAGGAGC AGCAGCAGCA GCAGGAGGAA GCCAGGCGGC GCGGCAGGA  
501 GCAGAGCCCA TGAACCCGA GAGCCGGCCT GGACCCTCGG GAATGAATGT  
551 TGGTCGAC (SEQ ID NO: 15)

**FIG. 6**



SalI

1	GTCGACGCCG	CCACCATGCC	GCCCAAAACC	CCCCGAAAAA	CGGCCGCCAC
		M P	P K T	P R K T	A A T
51	CGCCGCCGCT	GCCGCCGCGG	AACCCCCGGC	ACCGCCGCCG	CCGCCCCCTC
	A A A	A A A E	P P A	P P P	P P P P
101	CTGAGGAGGA	CCCAGAGCAG	GACAGCGGCC	CGGAGGACCT	GCCTCTCGTC
	E E D	P E Q	D S G P	E D L	P L V
151	AGGCTTGAGT	TTGAAGAAAC	AGAAGAACCT	GATTTTACTG	CATTATGTCA
	R L E F	E E T	E E P	D F T A	L C Q
201	GAAATTAAAG	ATACCAGATC	ATGTCAGAGA	GAGAGCTTGG	TTAACTTGGG
	K L K	I P D H	V R E	R A W	L T W E
251	AGAAAGTTTC	ATCTGTGGAT	GGAGTATTGG	GAGGTTATAT	TCAAAAGAAA
	K V S	S V D	G V L G	G Y I	Q K K
301	AAGGAACTGT	GGGGAATCTG	TATCTTTATT	GCACGAGTTG	ACCTAGATGA
	K E L W	G I C	I F I	A R V D	L D E
351	GATGTCGTTC	ACTTTACTGA	GCTACAGAAA	AACATACGAA	ATCAGTGTCC
	M S F	T L L S	Y R K	T Y E	I S V H
401	ATAAATTCTT	TAACTTACTA	AAAGAAATTG	ATACCAGTAC	CAAAGTTGAT
	K F F	N L L	K E I D	T S T	K V D
451	AATGCTATGT	CAAGACTGTT	GAAGAAGTAT	GATGTATTGT	TTGCACTCTT
	N A M S	R L L	K K Y	D V L F	A L F
501	CAGCAAATTG	GAAAGGACAT	GTGAACTTAT	ATATTTGACA	CAACCCAGCA
	S K L	E R T C	E L I	Y L T	Q P S S
551	GTTCGATATC	TACTGAAATA	AATTCTGCAT	TGGTGCTAAA	AGTTTCTTGG
	S I S	T E I	N S A L	V L K	V S W
601	ATCACATTTT	TATTAGCTAA	AGGGGAAGTA	TTACAAATGG	AAGATGATCT
	I T F L	L A K	G E V	L Q M E	D D L
651	GGTGATTTCA	TTTCAGTTAA	TGCTATGTGT	CCTTGACTAT	TTTATTAAAC
	V I S	F Q L M	L C V	L D Y	F I K L

FIG. 7A

701 TCTCACCTCC CATGTTGCTC AAAGAACCAT ATAAAACAGC TGTTATACCC  
       S P P M L L K E P Y K T A V I P  
 751 ATTAATGGTT CACCTCGAAC ACCCAGGCGA GGTCAGAACA GGAGTGCACG  
       I N G S P R T P R R G Q N R S A R  
 801 GATAGCAAAA CAACTAGAAA ATGATACAAG AATTATTGAA GTTCTCTGTA  
       I A K Q L E N D T R I I E V L C K  
 851 AAGAACATGA ATGTAATATA GATGAGGTGA AAAATGTTTA TTTCAAAAAT  
       E H E C N I D E V K N V Y F K N  
                                   EcoRI  
 901 TTTATACCTT TTATGAATTC TCTTGGACTT GTAACATCTA ATGGACTTCC  
       F I P F M N S L G L V T S N G L P  
 951 AGAGGTTGAA AATCTTTCTA AACGATACGA AGAAATTTAT CTTAAAAATA  
       E V E N L S K R Y E E I Y L K N K  
 1001 AAGATCTAGA TCGAAGATTA TTTTGGATC ATGATAAAAC TCTTCAGACT  
       D L D R R L F L D H D K T L Q T  
 1051 GATTCTATAG ACAGTTTGA AACACAGAGA ACACCACGAA AAAGTAACCT  
       D S I D S F E T Q R T P R K S N L  
 1101 TGATGAAGAG GTGAATATAA TTCCTCCACA CACTCCAGTT AGGACTGTTA  
       D E E V N I I P P H T P V R T V M  
 1151 TGAACACTAT CCAACAATTA ATGATGATTT TAAATTCTGC AAGTGATCAA  
       N T I Q Q L M M I L N S A S D Q  
 1201 CCTTCAGAAA ATCTGATTTC CTATTTTAAC AACTGCACAG TGAATCCAAA  
       P S E N L I S Y F N N C T V N P K  
 1251 AGAAAGTATA CTGAAAAGAG TGAAGGATAT AGGATACATC TTTAAAGAGA  
       E S I L K R V K D I G Y I F K E K  
 1301 AATTTGCTAA AGCTGTGGGA CAGGGTTGTG TCGAAATTGG ATCACAGCGA  
       F A K A V G Q G C V E I G S Q R  
 1351 TACAAACTTG GAGTTCGCTT GTATTACCGA GTAATGGAAT CCATGCTTAA  
       Y K L G V R L Y Y R V M E S M L K

FIG. 7B

1401 ATCAGAAGAA GAACGATTAT CCATTCAAAA TTTTAGCAAA CTTCTGAATG  
       S E E E R L S I Q N F S K L L N D  
 1451 ACAACATTTT TCATATGTCT TTATTGGCGT GCGCTCTTGA GGTGTGAATG  
       N I F H M S L L A C A L E V V M  
 1501 GCCACATATA GCAGAAGTAC ATCTCAGAAT CTTGATTCTG GAACAGATTT  
       A T Y S R S T S Q N L D S G T D L  
 1551 GTCTTTCCCA TGGATTCTGA ATGTGCTTAA TTTAAAAGCC TTTGATTTTT  
       S F P W I L N V L N L K A F D F Y  
 1601 ACAAAGTGAT CGAAAGTTTT ATCAAAGCAG AAGGCAACTT GACAAGAGAA  
       K V I E S F I K A E G N L T R E  
 1651 ATGATAAAAC ATTTAGAACG ATGTGAACAT CGAATCATGG AATCCCTTGC  
       M I K H L E R C E H R I M E S L A  
 1701 ATGGCTCTCA GATTCACCTT TATTTGATCT TATTAAACAA TCAAAGGACC  
       W L S D S P L F D L I K Q S K D R  
 1751 GAGAAGGACC AACTGATCAC CTTGAATCTG CTTGTCCTCT TAATCTTCCT  
       E G P T D H L E S A C P L N L P  
 1801 CTCCAGAATA ATCACACTGC AGCAGATATG TATCTTTCTC CTGTAAGATC  
       L Q N N H T A A D M Y L S P V R S  
 1851 TCCAAAGAAA AAAGGTTCAA CTACGCGTGT AAATTCTACT GCAAATGCAG  
       P K K K G S T T R V N S T A N A E  
 1901 AGACACAAGC AACCTCAGCC TTCCAGACCC AGAAGCCATT GAAATCTACC  
       T Q A T S A F Q T Q K P L K S T  
 1951 TCTCTTTCAC TGTTTTATAA AAAAGTGTAT CGGCTAGCCT ATCTCCGGCT  
       S L S L F Y K K V Y R L A Y L R L  
 2001 AAATACACTT TGTGAACGCC TTCTGTCTGA GCACCCAGAA TTAGAACATA  
       N T L C E R L L S E H P E L E H I  
 2051 TCATCTGGAC CCTTTTCCAG CACACCCTGC AGAATGAGTA TGAATCATG  
       I W T L F Q H T L Q N E Y E L M

FIG. 7C

2101 AGAGACAGGC ATTTGGACCA AATTATGATG TGTTCATGT ATGGCATATG  
       R D R H L D Q I M M C S M Y G I C  
 2151 CAAAGTGAAG AATATAGACC TTAAATTCAA AATCATTGTA ACAGCATACA  
       K V K N I D L K F K I I V T A Y K  
 2201 AGGATCTTCC TCATGCTGTT CAGGAGACAT TCAAACGTGT TTTGATCAAA  
       D L P H A V Q E T F K R V L I K  
 2251 GAAGAGGAGT ATGATTCTAT TATAGTATTC TATAACTCGG TCTTCATGCA  
       E E E Y D S I I V F Y N S V F M Q  
 2301 GAGACTGAAA ACAAATATTT TGCAGTATGC TTCCACCAGG CCCCCTACCT  
       R L K T N I L Q Y A S T R P P T L  
 2351 TGTCACCAAT ACCTCACATT CCTCGAAGCC CTTACAAGTT TCCTAGTTCA  
       S P I P H I P R S P Y K F P S S  
 2401 CCCTTACGGA TTCCTGGAGG GAACATCTAT ATTTCACCCC TGAAGAGTCC  
       P L R I P G G N I Y I S P L K S P  
 2451 ATATAAAATT TCAGAAGGTC TGCCAACACC AACAAAAATG ACTCCAAGAT  
       Y K I S E G L P T P T K M T P R S  
 2501 CAAGAATCTT AGTATCAATT GGTGAATCAT TCGGGACTTC TGAGAAGTTC  
       R I L V S I G E S F G T S E K F  
 2551 CAGAAAATAA ATCAGATGGT ATGTAACAGC GACCGTGTGC TCAAAAGAAG  
       Q K I N Q M V C N S D R V L K R S  
 2601 TGCTGAAGGA AGCAACCCTC CTAAACCACT GAAAAAACTA CGCTTTGATA  
       A E G S N P P K P L K K L R F D I  
 2651 TTGAAGGATC AGATGAAGCA GATGGAAGTA AACATCTCCC AGGAGAGTCC  
       E G S D E A D G S K H L P G E S  
 2701 AAATTTTCAGC AGAAACTGGC AGAAATGACT TCTACTCGAA CACGAATGCA  
       K F Q Q K L A E M T S T R T R M Q  
 2751 AAAGCAGAAA ATGAATGATA GCATGGATAC CTCAAACAAG GAAGAGAAAT  
       K Q K M N D S M D T S N K E E K \*

NotI

2801 GAGGATCTCA GGACCGGCGG CCGC

FIG. 7D

EcoRI  
 1 GAATTCGCCG CCACCATGAC CATGGACTCT GGAGCAGACA ACCAGCAGAG  
                                   M T M D S G A D N Q Q S  
 51 TGGAGATGCA GCTGTAACAG AAGCTGAAAA CCAACAAATG ACAGTTCAAG  
           G D A A V T E A E N Q Q M T V Q A  
 101 CCCAGCCACA GATTGCCACA TTAGCCCAGG TATCTATGCC AGCAGCTCAT  
           Q P Q I A T L A Q V S M P A A H  
 151 GCAACATCAT CTGCTCCAC CGTAACTCTA GTACAGCTGC CCAATGGGCA  
           A T S S A P T V T L V Q L P N G Q  
 201 GACAGTTCAA GTCCATGGAG TCATTGAGGC GGCCCAGCCA TCAGTTATTC  
           T V Q V H G V I Q A A Q P S V I Q  
 251 AGTCTCCACA AGTCCAAACA GTTCAGATTT CAACTATTGC AGAAAGTGAA  
           S P Q V Q T V Q I S T I A E S E  
 301 GATTCACAGG AGTCAGTGGA TAGTGTA ACT GATTCCCAA AGCGAAGGGA  
           D S Q E S V D S V T D S Q K R R E  
 351 AATTCTTTCA AGGAGGCCTT CCTTCAGGAA AATTTTGAAT GACTTATCTT  
           I L S R R P S F R K I L N D L S S  
 401 CTGATGCACC AGGAGTGCCA AGGATTGAAG AAGAGAAGTC TGAAGAGGAG  
           D A P G V P R I E E E K S E E E  
 451 GCTTCAGCAC CTGCCATCAC CGCTGTAGCG GTGCCAACGC CAATTTACCG  
           A S A P A I T A V A V P T P I Y R  
 501 GACTAGCAGT GGACAGTATA TTACCATTAC CCAGAGAGGA GCAATACAGC  
           T S S G Q Y I T I T Q R G A I Q L  
 551 TGGCTAGCAA TGGTACCGAT GGGGTACAGG GCCTGCAAAC ATTAACCATG  
           A S N G T D G V Q G L Q T L T M  
 601 GCCAATGCAG CAGCCACTCA GCCGGGTACT ACCATTCTAC AGTATGCACA  
           A N A A A T Q P G T T I L Q Y A Q  
 651 GACCACTGAT GGACAGCAGA TCTTAGTGCC CAGCAACCAA GTTGTGTGTC  
           T T D G Q Q I L V P S N Q V V V Q

FIG. 8A

701 AAGCTGCCTC TGGAGACGTA CAAACATACC AGATTTCGCAC AGCACCCACT  
       A A S G D V Q T Y Q I R T A P T  
 751 AGCACTATTG CCCCTGGAGT TGTATGGCA TCCTCCCCAG CACTTCCTAC  
       S T I A P G V V M A S S P A L P T  
 801 ACAGCCTGCT GAAGAAGCAG CACGAAAGAG AGAGGTCCGT CTAATGAAGA  
       Q P A E E A A R K R E V R L M K N  
 851 ACAGGGAAGC AGCTCGTGAG TGTCGTAGAA AGAAGAAAGA ATATGTGAAA  
       R E A A R E C R R K K K E Y V K  
 901 TGTTTAGAAA ACAGAGTGGC AGTGCTTGAA AATCAAAACA AGACATTGAT  
       C L E N R V A V L E N Q N K T L I  
 951 TGAGGAGCTA AAAGCACTTA AGGACCTTTA CTGCCACAAA TCAGATTAAT  
       E E L K A L K D L Y C H K S D \*  
           SalI  
 1001 TTGGGTCGAC

**FIG. 8B**



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1  aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
   HindIII      M R H I I C H G G V I
51  cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
   T E E M A A S L L D Q L I E E V L
101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
   A D N L P P P S H F E P P T L H E
151 ctgtatgatt tagacgtgac ggccccgaa gatcccaacg aggaggcgg
   L Y D L D V T A P E D P N E E A
201 ttcgcagatt tttcccgact ctgtaatggt ggcggtgcag gaagggattg
   V S Q I F P D S V M L A V Q E G I
251 acttactcac ttttccgccg gcgccccggt ctccggagcc gcctcacctt
   D L L T F P P A P G S P E P P H L
301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
   S R Q P E Q P E Q R A L G P V S
351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
   M P N L V P E V I D L T C H E A G
401 ttccaccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
   F P P S D D E D E E G E E F V L D
451 tatgtggagc accccgggca cggttgcagg tcttgtcatt atcaccggag
   Y V E H P G H G C R S C H Y H R
501 gaatacgggg gaccagata ttatgtgttc gctttgctat atgaggacct
   R N T G D P D I M C S L C Y M R T
551 gtggcatggt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
   C G M F V Y S P V S E P E P E P E
601 ccagaaccgg agcctgcaag acctaccgc cgtcctaaaa tggcgccctgc
   P E P E P A R P T R R P K M A P
651 taccctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
   A I L R R P T S P V S R E C N S S
701 cggatagctg tgactccggt ccttctaaca cacctcctga gatacaccgc
   T D S C D S G P S N T P P E I H P
751 gtgggtccgc tgtgccccat taaaccagtt gccgtgagag ttgggtgggcg
   V V P L C P I K P V A V R V G G
801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
   R R Q A V E C I E D L L N E P G Q
851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
   P L D L S C K R P R P - XhoI

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**Figure 10.** Nucleotide coding sequence of E1a cDNA (SEQ ID NO: 40). Cloning sites HindIII and XhoI, and two amino acid residue positions Y47 and C124 are underscored.



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1  aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
   HindIII           M R H I I C H G G V I

51  cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
   T E E M A A S L L D Q L I E E V L

101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
   A D N L P P P S H F E P P T L H E

151 ctgcatgatt tagacgtgac ggcccccgaa gatcccaacg aggaggcggt
   L H D L D V T A P E D P N E E A

201 ttgcgagatt tttcccgact ctgtaatggt ggcggtgcag gaagggattg
   V S Q I F P D S V M L A V Q E G I

251 acttactcac ttttccgccc gcgccccggt ctccggagcc gcctcacctt
   D L L T F P P A P G S P E P P H L

301 tccccggcagc ccgagcagcc ggagcagaga gccttgsggtc cggtttctat
   S R Q P E Q P E Q R A L G P V S

351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
   M P N L V P E V I D L T C H E A G

401 ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
   F P P S D D E D E E G E E F V L D

451 tatgtggagc accccgggca cggttgagg tcttgtcatt atcaccggag
   Y V E H P G H G C R S C H Y H R

501 gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
   R N T G D P D I M C S L C Y M R T

551 gtggcatggt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
   C G M F V Y S P V S E P E P E P E

601 ccagaaccgg agcctgcaag acctaccgcg cgtcctaaaa tggcgccctgc
   P E P E P A R P T R R P K M A P

651 taccctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
   A I L R R P T S P V S R E C N S S

701 cggatagctg tgactccggt ccttctaaca cacctcctga gatacacccg
   T D S C D S G P S N T P P E I H P

751 gtggtcccg cgtgccccat taaaccagtt gccgtgagag ttggtgggcg
   V V P L C P I K P V A V R V G G

801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
   R R Q A V E C I E D L L N E P G Q

851 ctttggactt gagctgtaaa cgccccaggg cataactcga g
   P L D L S C K R P R P - XhoI

```

**Figure 11. Nucleotide coding sequence of E1a\_Y47H (SEQ ID NO: 41). Cloning sites HindIII and XhoI are underscored.**

```

1  aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
   HindIII M T M E S G A D N Q Q
51  tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
   S G D A A V T E A E N Q Q M T A Q
101  cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
   A Q P Q I A T L A Q V S M P A A H
151  gcgacatcat ctgctcccac tgtaacctta gtgcagctgc ccaatgggca
   A T S S A P T V T L V Q L P N G
201  gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
   Q T V Q V H G V I Q A A Q P S V I
251  agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
   Q S P Q V Q T V Q S S C K D L K R
301  cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
   L F S G T Q I S T I A E S E D S
351  ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
   Q E S V D S V T D S Q K R R E I L
401  caaggaggcc ttcctacagg aaaattttga atgacttatc ttctgatgca
   S R R P S Y R K I L N D L S S D A
451  ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
   P G V P R I E E E K S E E E T S
501  ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
   A P A I T T V T V P T P I Y Q T S
551  gtgggcagta tattgccatt acccaggagg gagctataca gctggctaac
   S G Q Y I A I T Q G G A I Q L A N
601  aatgggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
   N G T D G V Q G L Q T L T M T N
651  agctgccact cagccgggta ccactattct acagtatgca cagaccactg
   A A A T Q P G T T I L Q Y A Q T T
701  atggacagca gattctagtg ccagcaacc aagttgttgt tcaagctgcc
   D G Q Q I L V P S N Q V V V Q A A
751  tctggcgatg tacaacata ccaattcgt acagcaccca ctagcaccat
   S G D V Q T Y Q I R T A P T S T
801  cgcccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
   I A P G V V M A S S P A L P T Q P
851  ctgaagaagc agcccggaag agagaggttc gtctaataaa gaacagggaa
   A E E A A R K R E V R L M K N R E
901  gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
   A A R E C R R K K K E Y V K C L
951  gaacagagtg gcagtgcctg aaaacaaaa caagacattg attgaggagc
   E N R V A V L E N Q N K T L I E E
1001  taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
      L K A L K D L Y C H K S D BamHI

```

Figure 12. Nucleotide coding sequence of hamster CREB-B cDNA (SEQ ID NO: 42). Cloning sites HindIII and BamHI are underscored.

```

1  aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
   HindIII           M T M E S G A D N Q Q
51  tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
   S G D A A V T E A E N Q Q M T A Q
101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
   A Q P Q I A T L A Q V S M P A A H
151 gcgacatcat ctgctccacac tgtaacctta gtgcagctgc ccaatgggca
   A T S S A P T V T L V Q L P N G
201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
   Q T V Q V H G V I Q A A Q P S V I
251 agtctccaca agtccaaaca gttcagtcct cctgtaagga cttaaaaaga
   Q S P Q V Q T V Q S S C K D L K R
301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
   L F S G T Q I S T I A E S E D S
351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
   Q E S V D S V T D S Q K R R E I L
401 caaggaggcc ttcctccagg aaaattttga atgacttatc ttctgatgca
   S R R P S F R K I L N D L S S D A
451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
   P G V P R I E E E K S E E E T S
501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
   A P A I T T V T V P T P I Y Q T S
551 gtgggacagta tattgccatt acccagggag gagctataca gctggctaac
   S G Q Y I A I T Q G G A I Q L A N
601 aatgggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
   N G T D G V Q G L Q T L T M T N
651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
   A A A T Q P G T T I L Q Y A Q T T
701 atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
   D G Q Q I L V P S N Q V V V Q A A
751 tctggcgatg taaaaacata ccaaattcgt acagcaccca ctagcaccat
   S G D V Q T Y Q I R T A P T S T
801 cgccccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
   I A P G V V M A S S P A L P T Q P
851 ctgaagaagc agcccgggag agagagggtc gtctaataaa gaacagggaa
   A E E A A R K R E V R L M K N R E
901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
   A A R E C R R K K K E Y V K C L
951 gaacagagtg gcagtgcctg aaaacacaaa caagacattg attgaggagc
   E N R V A V L E N Q N K T L I E E
1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
      L K A L K D L Y C H K S D - BamHI

```

Figure 13. Nucleotide coding sequence of hamster CREB-B Y134F cDNA (SEQ ID NO: 43). Cloning sites HindIII and BamHI are underscored.

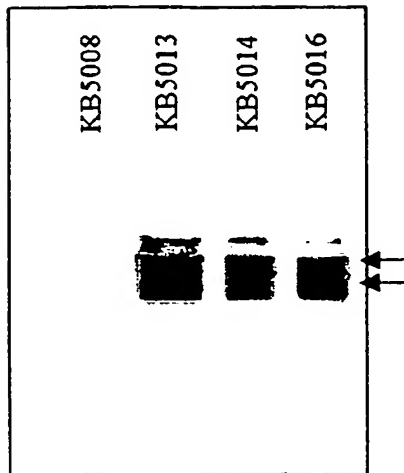
1 aagcttactg ttggtaaagc cgccaccatg gaggcttggg agtgtttgga  
    HindIII  M E A W E C L  
 51 agatTTTTct gctgtgcgta acttgctgga acagagctct aacagtacct  
    E D F S A V R N L L E Q S S N S T  
 101 cttggTTTTg gaggtttctg tggggctcat cccaggcaaa gttagtctgc  
    S W F W R F L W G S S Q A K L V C  
 151 agaattaagg aggattacaa gtgggaattt gaagagcttt tgaaatcctg  
    R I K E D Y K W E F E E L L K S  
 201 tggtgagctg tttgattctt tgaatctggg tcaccaggcg cttttccaag  
    C G E L F D S L N L G H Q A L F Q  
 251 agaaggtcat caagactttg gatttttcca caccggggcg cgctgcggct  
    E K V I K T L D F S T P G R A A A  
 301 gctgttgctt ttttgagttt tataaaggat aaatggagcg aagaaaccca  
    A V A F L S F I K D K W S E E T  
 351 tctgagcggg gggtacctgc tggattttct ggccatgcat ctgtggagag  
    H L S G G Y L L D F L A M H L W R  
 401 cggttgtgag acacaagaat cgcttgctac tgttgcttcc cgtccgcccg  
    A V V R H K N R L L L L S S V R P  
 451 gcgataatac cgacggagga gcagcagcag cagcaggagg aagccaggcg  
    A I I P T E E Q Q Q Q Q E E A R  
 501 gcggcggcag gagcagagcc catggaaccc gagagccggc ctggaccctc  
    R R R Q E Q S P W N P R A G L D P  
 551 gggaatgatc taga  
    R E - XbaI

Figure 14. Nucleotide coding sequence of E1b-19K (SEQ ID NO: 44). Cloning sites HindIII and XbaI are underscored.

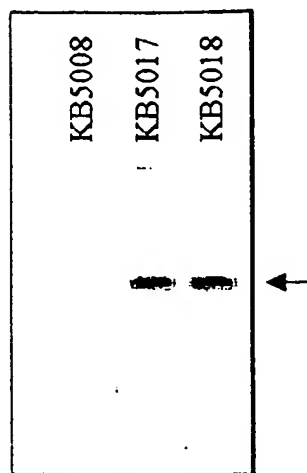
<sup>NcoI</sup>  
1    ccatgggctca agctgggaga acaggggtatg ataaccgaga gatcgtgatg  
     M   A   Q   A   G   R   T   G   Y   D   N   R   E   I   V   M  
51    aagtacatcc attataagct gtcacagagg ggctacgagt gggatgtggg  
     K   Y   I   H   Y   K   L   S   Q   R   G   Y   E   W   D   V  
101   agatgtggac gccgcggcgg cggccgcgag ccccggtgcca cctgtgggtcc  
     G   D   V   D   A   A   A   A   A   A   S   P   V   P   P   V   V  
151   acctgaccct ccgccgggct ggggatgact tctcccgtcg ctaccgtcgc  
     H   L   T   L   R   R   A   G   D   D   F   S   R   R   Y   R   R  
201   gacttcgagg agatgtccag tcagctgcac ctgacgccct tcaccgcgag  
     D   F   A   E   M   S   S   Q   L   H   L   T   P   F   T   A  
251   gggacgcttt gctacgggtg tggaggaact cttcagggat ggggtgaact  
     R   G   R   F   A   T   V   V   E   E   L   F   R   D   G   V   N  
301   gggggaggat tgtggccttc tttgagttcg gtgggggtcat gtgtgtggag  
     W   G   R   I   V   A   F   F   E   F   G   G   V   M   C   V   E  
351   agcgtcaaca gggagatgtc acccctggtg gacaacatcg ccctgtggat  
     S   V   N   R   E   M   S   P   L   V   D   N   I   A   L   W  
401   gaccgagtac ctgaaccggc atctgcacac ctggatccag gataacggag  
     M   T   E   Y   L   N   R   H   L   H   T   W   I   Q   D   N   G  
451   gctgggacgc atttgtggaa ctgtacggcc ccagtgtgag gcctctgttt  
     G   W   D   A   F   V   E   L   Y   G   P   S   V   R   P   L   F  
501   gatttctctt ggctgtctct gaagaccctg ctcagcctgg ccctgggtcgg  
     D   F   S   W   L   S   L   K   T   L   L   S   L   A   L   V  
551   ggcctgcata actctgggta cctacctggg ccacaagtga tctaga  
     G   A   C   I   T   L   G   T   Y   L   G   H   K   -   XbaI

**Figure 15. Nucleotide coding sequence of hamster Bcl2 deletion mutant (SEQ ID NO: 45). Cloning sites NcoI and XbaI are underscored.**

a) E1a (31 KD)



b) CREB (35 KD)



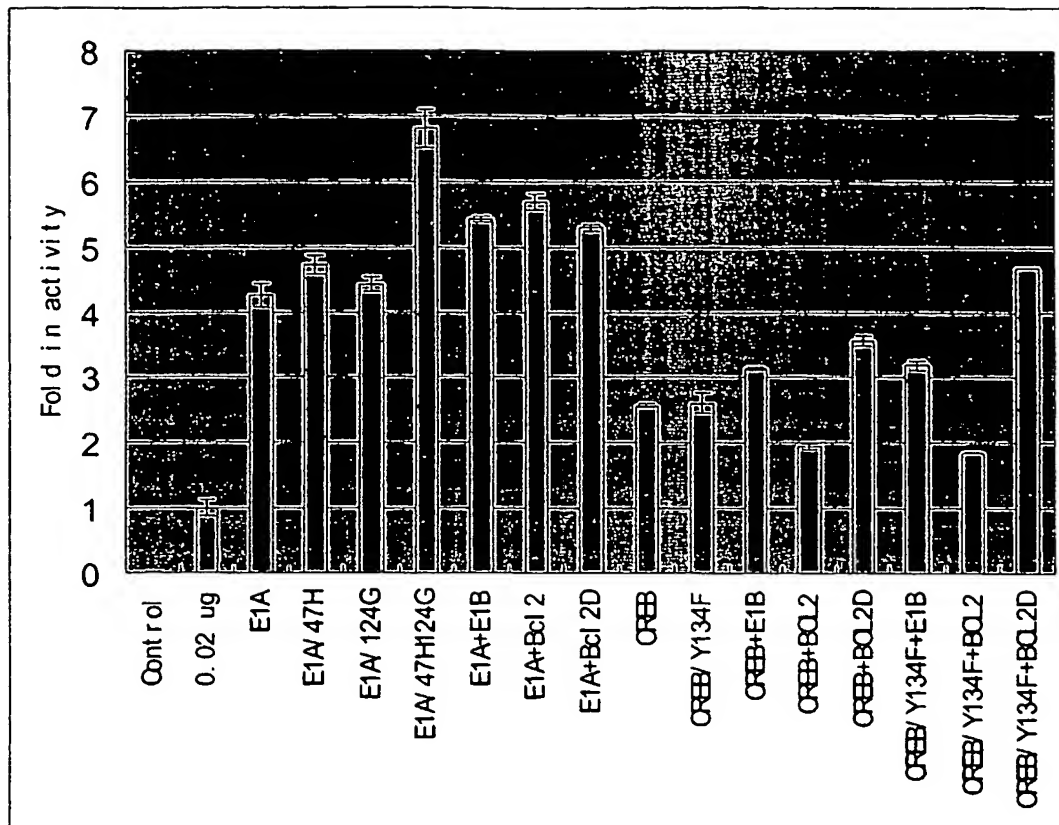
c) Bcl2 (26 KD)



**Figure 16. Western blots of E1a, CREB and Bcl2.**

In a), b), and c),  $1 \times 10^5$  CHO-K1 cells were transfected with 0.4  $\mu$ g of indicated plasmid DNA. Cell lysates were collected after 48 hours and probed with appropriate antibodies. KB5008 transfected cells were used as negative controls.

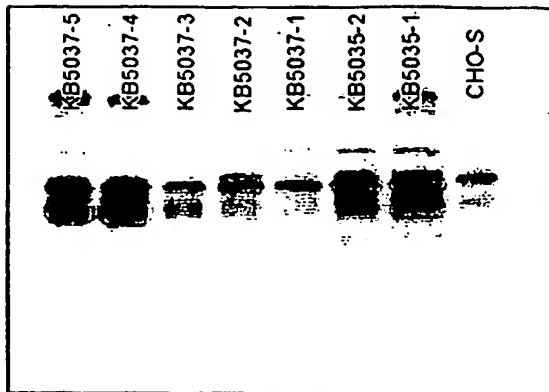
BEST AVAILABLE COPY



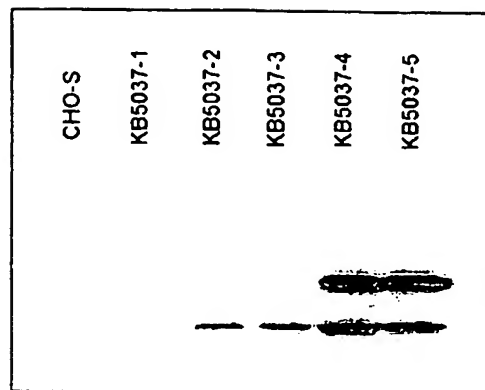
**Figure 17. E1a and CREB enhanced CMV promoter in CHO-K1 cells.**

$1 \times 10^5$  cells were transfected with 0.02  $\mu$ g of SEAP reporter construct KB5019 and 0.2  $\mu$ g of E1a or CREB expressing constructs. Total DNA was added up to 0.4  $\mu$ g/well by control plasmid KB5008, E1b-19K or Bcl2 expressing plasmids. SEAP activities from culture media were assay 48 hours after transfection. The control was mock transfected CHO-K1 cells.

a) CREB (35 KD)



b) Bcl2D (22KD)



**Figure 18. Western blots showing overexpression of hamster CREB-B Y134F and hamster  $\Delta$ Bcl-2 in stable transfectant CHO-S cell lines.**